
Methods to quantify microRNAs in the Myc gene network for posttranscriptional gene repression.

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Public Summary:

As a global transcription factor, Myc regulates both protein-coding genes and noncoding microRNA genes. Myc-activated or repressed miRNAs are involved in various pathways to affect tumorigenesis, mediate apoptosis, proliferation, angiogenesis, metastasis, and metabolism downstream of Myc. Functional characterization of miRNAs in the Myc network requires the accurate detection and quantification of miRNA expression levels. Here, we describe two widely used methodologies to determine miRNA expression, including miRNA real-time PCR and miRNA northern analysis.

Scientific Abstract:

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